

## SEQUENCE LISTING

&lt;110&gt; University of Rochester

Chang, Chawnshang

&lt;120&gt; Hydroxyflutamide Induced Pathways

Related to Androgen Receptor Negative Prostate Cancer Cells

&lt;130&gt; 21108.0017P1

&lt;150&gt; 60/423,340

&lt;151&gt; 2002-10-31

&lt;150&gt; PCT/US02/11086

&lt;151&gt; 2002-04-05

&lt;150&gt; 60/365,060

&lt;151&gt; 2002-03-13

&lt;150&gt; 60/282,266

&lt;151&gt; 2001-04-06

&lt;160&gt; 28

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 1587

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 1

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tgctccctc	ccccatcaaa	ggaaaggggg	aaatgtctca	gtcgaaaggc	aagaagcgaa	300
accctggcct	taaaattcca	aaagaagcat	ttgaacaacc	tcagaccagt	tccacaccac	360
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aacatccatt	tttcacccta	catgaatcca	aaggaaacaga	tgtggcatct	tttgtaaaac	1260
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&lt;210&gt; 2

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 2

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20     25     30
Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val
35     40     45
Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr
50     55     60
Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala
65     70     75     80
Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu
85     90     95
Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr
100    105    110
Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys
115    120    125
Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile
130    135    140
Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val
145    150    155    160
Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile
165    170    175
His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln
180    185    190
Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val
195    200    205
Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg
210    215    220
Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile
225    230    235    240
Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro
245    250    255
Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu
260    265    270
Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val
275    280    285
Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr
290    295    300
Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys
305    310    315    320
Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp
325    330

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<210> 3  
 <211> 3080  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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 gctactgaca gcttctcagg caggttcgaa gatgtctatc agctgcagga ggatgtgctg 180  
 ggggaagggtg ctcacgctcg tgtgcagacc tgtgtcaatc tcatcaccaa ccaggaatat 240  
 gctgtcaaga tcattgagaa gcagctgggc cacatccgca gcagggtgtt ccgggagggtg 300  
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 gaggaggacc gtttctacct ggtgtttgag aagatgcgtg gcggatccat cctaagccac 420  
 atccatagaa ggcgccactt taacgagctg gaggccagcg tggtagtaca ggacgtggcc 480  
 agtgccttgg acttctctga taacaaaggc atcgcccaca gggacctaaa gccagagaac 540  
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 atctacgaca agcgtgcga cctgtggagc ctgggcgtca tctctacat cctgcttagt 780  
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3080

&lt;210&gt; 4

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 4

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Arg	Lys	Lys	Lys	Arg	Cys	Arg	Ala	Thr	Asp	Ser	Phe	Ser	Gly	Arg	Phe	20	25	30	
Glu	Asp	Val	Tyr	Gln	Leu	Gln	Glu	Asp	Val	Leu	Gly	Glu	Gly	Ala	His	35	40	45	
Ala	Arg	Val	Gln	Thr	Cys	Val	Asn	Leu	Ile	Thr	Asn	Gln	Glu	Tyr	Ala	50	55	60	
Val	Lys	Ile	Ile	Glu	Lys	Gln	Leu	Gly	His	Ile	Arg	Ser	Arg	Val	Phe	65	70	75	80
Arg	Glu	Val	Glu	Met	Leu	Tyr	Gln	Cys	Gln	Gly	His	Arg	Asn	Val	Leu	85	90	95	
Glu	Leu	Ile	Glu	Phe	Phe	Glu	Glu	Glu	Asp	Arg	Phe	Tyr	Leu	Val	Phe	100	105	110	
Glu	Lys	Met	Arg	Gly	Gly	Ser	Ile	Leu	Ser	His	Ile	His	Arg	Arg	Arg	115	120	125	
His	Phe	Asn	Glu	Leu	Glu	Ala	Ser	Val	Val	Val	Gln	Asp	Val	Ala	Ser	130	135	140	
Ala	Leu	Asp	Phe	Leu	His	Asn	Lys	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	145	150	155	160
Pro	Glu	Asn	Ile	Leu	Cys	Glu	His	Pro	Asn	Gln	Val	Ser	Pro	Val	Lys	165	170	175	
Ile	Cys	Asp	Phe	Asp	Leu	Gly	Ser	Gly	Ile	Lys	Leu	Asn	Gly	Asp	Cys	180	185	190	
Ser	Pro	Ile	Ser	Thr	Pro	Glu	Leu	Leu	Thr	Pro	Cys	Gly	Ser	Ala	Glu	195	200	205	
Tyr	Met	Ala	Pro	Glu	Val	Val	Glu	Ala	Phe	Ser	Glu	Glu	Ala	Ser	Ile	210	215	220	
Tyr	Asp	Lys	Arg	Cys	Asp	Leu	Trp	Ser	Leu	Gly	Val	Ile	Leu	Tyr	Ile	225	230	235	240
Leu	Leu	Ser	Gly	Tyr	Pro	Pro	Phe	Val	Gly	His	Cys	Gly	Ser	Asp	Cys	245	250	255	
Gly	Trp	Asp	Arg	Gly	Glu	Ala	Cys	Pro	Ala	Cys	Gln	Asn	Met	Leu	Phe	260	265	270	
Glu	Ser	Ile	Gln	Glu	Gly	Lys	Tyr	Glu	Phe	Pro	Asp	Lys	Asp	Trp	Ser	275	280	285	
His	Ile	Ser	Phe	Ala	Ala	Lys	Asp	Leu	Ile	Ser	Lys	Leu	Leu	Val	Arg	290	295	300	
Asp	Ala	Lys	Gln	Arg	Leu	Ser	Ala	Ala	Gln	Val	Leu	Gln	His	Pro	Trp	305	310	315	320
Val	Gln	Gly	Cys	Ala	Pro	Glu	Asn	Thr	Leu	Pro	Thr	Pro	Leu	Val	Leu	325	330	335	
Gln	Arg	Asn	Ser	Cys	Ala	Lys	Asp	Leu	Thr	Ser	Phe	Ala	Ala	Glu	Ala	340	345	350	
Ile	Ala	Met	Asn	Arg	Gln	Leu	Ala	Gln	Cys	Glu	Glu	Asp	Ala	Gly	Gln	355	360	365	
Asp	Gln	Pro	Val	Val	Ile	Arg	Ala	Thr	Ser	Arg	Cys	Leu	Gln	Leu	Ser	370	375	380	

Pro Pro Ser Gln Ser Lys Leu Ala Gln Arg Arg Gln Arg Ala Ser Leu  
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 Ser Ala Thr Pro Val Val Leu Val Gly Asp Arg Ala  
 405 410

<210> 5  
 <211> 1096  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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<210> 6  
 <211> 232  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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 20 25 30  
 Leu Leu Arg Arg Tyr Pro Leu Glu Asp His Pro Glu Phe Pro Leu Pro  
 35 40 45  
 Pro Asp Val Val Phe Phe Cys Gln Pro Glu Gly Cys Leu Ser Val Arg  
 50 55 60  
 Gln Arg Arg Met Ser Leu Arg Asp Asp Thr Ser Phe Val Phe Thr Leu  
 65 70 75 80  
 Thr Asp Lys Asp Thr Gly Val Thr Arg Tyr Gly Ile Cys Val Asn Phe  
 85 90 95  
 Tyr Arg Ser Phe Gln Lys Arg Met Pro Lys Glu Lys Val Glu Gly Gly  
 100 105 110  
 Ala Gly Pro Arg Gly Lys Glu Gly Ala His Thr Ser Gly Ala Ser Glu  
 115 120 125

Glu Ala Ala Ala Gly Ser Ser Glu Ser Gly Ser Thr Leu Gln Pro Pro  
 130 135 140  
 Ser Ala Asp Ser Thr Pro Asp Val Asn Gln Ser Pro Arg Gly Lys Arg  
 145 150 155 160  
 Arg Ala Lys Ala Gly Ser Arg Ser Arg Asn Ser Thr Leu Thr Ser Leu  
 165 170 175  
 Cys Val Leu Ser His Tyr Pro Phe Phe Ser Thr Phe Arg Glu Cys Leu  
 180 185 190  
 Tyr Thr Leu Lys Arg Leu Val Asp Cys Cys Ser Glu Arg Leu Leu Gly  
 195 200 205  
 Lys Lys Leu Gly Ile Pro Arg Gly Val Gln Arg Tyr Gly Leu Leu Leu  
 210 215 220  
 Val Leu Gly Arg Thr Leu Arg Asp  
 225 230

<210> 7  
 <211> 7161  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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&lt;210&gt; 8

&lt;211&gt; 1563

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 8

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20          25          30
Ser Gly Arg Ala Gly Thr Trp Pro Arg Gly Pro Ser Glu Cys Ser Pro
35          40          45
Arg Glu Lys Met Ala Ala Ala Ala Gly Asn Arg Ala Ser Ser Ser Gly
50          55          60
Phe Pro Gly Ala Arg Ala Thr Ser Pro Glu Ala Gly Gly Gly Gly Gly
65          70          75          80
Ala Leu Lys Ala Ser Ser Ala Pro Ala Ala Ala Gly Leu Leu Arg
85          90          95
Glu Ala Gly Ser Gly Gly Arg Glu Arg Ala Asp Trp Arg Arg Arg Gln
100         105         110
Leu Arg Lys Val Arg Ser Val Glu Leu Asp Gln Leu Pro Glu Gln Pro
115         120         125
Leu Phe Leu Ala Ala Ser Pro Pro Ala Ser Ser Thr Ser Pro Ser Pro
130         135         140
Glu Pro Ala Asp Ala Ala Gly Ser Gly Thr Gly Phe Gln Pro Val Ala
145         150         155         160
Val Pro Pro Pro His Gly Ala Ala Ser Arg Gly Gly Ala His Leu Thr
165         170         175
Glu Ser Val Ala Ala Pro Asp Ser Gly Ala Ser Ser Pro Ala Ala Ala
180         185         190

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Glu Pro Gly Glu Lys Arg Ala Pro Ala Ala Glu Pro Ser Pro Ala Ala  
 195 200 205  
 Ala Pro Ala Gly Arg Glu Met Glu Asn Lys Glu Thr Leu Lys Gly Leu  
 210 215 220  
 His Lys Met Asp Asp Arg Pro Glu Glu Arg Met Ile Arg Glu Lys Leu  
 225 230 235 240  
 Lys Ala Thr Cys Met Pro Ala Trp Lys His Glu Trp Leu Glu Arg Arg  
 245 250 255  
 Asn Arg Arg Gly Pro Val Val Val Lys Pro Ile Pro Val Lys Gly Asp  
 260 265 270  
 Gly Ser Glu Met Asn His Leu Ala Ala Glu Ser Pro Gly Glu Val Gln  
 275 280 285  
 Ala Ser Ala Ala Ser Pro Ala Ser Lys Gly Arg Arg Ser Pro Ser Pro  
 290 295 300  
 Gly Asn Ser Pro Ser Gly Arg Thr Val Lys Ser Glu Ser Pro Gly Val  
 305 310 315 320  
 Arg Arg Lys Arg Val Ser Pro Val Pro Phe Gln Ser Gly Arg Ile Thr  
 325 330 335  
 Pro Pro Arg Arg Ala Pro Ser Pro Asp Gly Phe Ser Pro Tyr Ser Pro  
 340 345 350  
 Glu Glu Thr Asn Arg Arg Val Asn Lys Val Met Arg Ala Arg Leu Tyr  
 355 360 365  
 Leu Leu Gln Gln Ile Gly Pro Asn Ser Phe Leu Ile Gly Gly Asp Ser  
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 Pro Asp Asn Lys Tyr Arg Val Phe Ile Gly Pro Gln Asn Cys Ser Cys  
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 Ala Arg Gly Thr Phe Cys Ile His Leu Leu Phe Val Met Leu Arg Val  
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 420 425 430  
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 Ser Arg Ile Lys Ala Pro Ser Arg Asn Thr Ile Gln Lys Phe Val Ser  
 450 455 460  
 Arg Met Ser Asn Ser His Thr Leu Ser Ser Ser Thr Ser Thr Ser  
 465 470 475 480  
 Ser Ser Glu Asn Ser Ile Lys Asp Glu Glu Glu Gln Met Cys Pro Ile  
 485 490 495  
 Cys Leu Leu Gly Met Leu Asp Glu Glu Ser Leu Thr Val Cys Glu Asp  
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 Gly Cys Arg Asn Lys Leu His His His Cys Met Ser Ile Trp Ala Glu  
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 Glu Cys Arg Arg Asn Arg Glu Pro Leu Ile Cys Pro Leu Cys Arg Ser  
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 Lys Trp Arg Ser His Asp Phe Tyr Ser His Glu Leu Ser Ser Pro Val  
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 Asp Ser Pro Ser Ser Leu Arg Ala Ala Gln Gln Gln Thr Val Gln Gln  
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 Gln Pro Leu Ala Gly Ser Arg Arg Asn Gln Glu Ser Asn Phe Asn Leu  
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 Thr His Tyr Gly Thr Gln Gln Ile Pro Pro Ala Tyr Lys Asp Leu Ala  
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 Glu Pro Trp Ile Gln Val Phe Gly Met Glu Leu Val Gly Cys Leu Phe  
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 Ser Gly Gly Ser Ser Gly Ser Ser Pro Ser Gly Gly Ala Thr Ser Gly  
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Ser Ser Gln Thr Ser Ile Ser Gly Asp Val Val Glu Ala Cys Cys Ser  
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 Val Leu Ser Met Val Cys Ala Asp Pro Val Tyr Lys Val Tyr Val Ala  
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 885 890 895  
 Ser Thr His Phe Thr Arg Met Arg Arg Arg Leu Met Ala Ile Ala Asp  
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 Leu Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu  
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 Leu Leu Lys His Pro Val Phe Arg Thr Thr Trp  
 1555 1560

&lt;210&gt; 9

&lt;211&gt; 3621

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 9

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tgccttattc	agggaaggag	gagcctgtcc	tgctgtggc	catgaccctg	cctctcccag	2940
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ttgtctctgt	tttacaagtt	ggagtcactc	ttatgctgta	cccagtttct	aaactggaga	3060
ctgtgtgtgc	cctctgggct	ctgagtaccc	ctgctttggg	cttgggccta	ggctgcattg	3120
aaaagagctg	aaggttgtgg	cctttgcgct	cctggcccag	cctttgttcc	ccactggagc	3180
agaaggggag	atggacgaca	cggtcggggc	atctggcctg	gccagtgcgc	tgatcccaga	3240
gagcccagg	aggtgtctca	ggctgcctga	gtcgtgacct	gctaggccag	agcccactcc	3300
atctgggtga	agggaaagcc	catatgctac	caccagctgt	gtccaaaacc	gccagctctg	3360
ttcttctca	gccagcctcg	cccatcccc	tgaggtctca	gcccctttcc	cttgtagctg	3420
ctccccctga	gggggaaatg	cagcaggggt	tgggaaaaca	gcactctcaa	gcagattaga	3480
ggtggccata	tttacctcag	cctggggcgt	ggtcctttct	tccggccctt	cccctccaaa	3540

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 aaagaaaaaa aaaaaaaaaa a

3600  
 3621

<210> 10  
 <211> 657  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 10  
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 Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys  
 20 25 30  
 Asn Lys Asp Thr Gly His Ser Asn Arg Gln Lys Lys His Asn Ser Ser  
 35 40 45  
 Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser Cys Ala  
 50 55 60  
 Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile Lys Phe  
 65 70 75 80  
 Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Lys  
 85 90 95  
 Tyr Glu Asp Val Glu His Lys Val Thr Val Phe Gly Gln Pro Leu  
 100 105 110  
 Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln  
 115 120 125  
 Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met  
 130 135 140  
 Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser  
 145 150 155 160  
 Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser  
 165 170 175  
 Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg  
 180 185 190  
 Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro  
 195 200 205  
 Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly  
 210 215 220  
 Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser  
 225 230 235 240  
 Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser  
 245 250 255  
 Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg  
 260 265 270  
 Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln Glu  
 275 280 285  
 Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly Gly  
 290 295 300  
 Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser  
 305 310 315 320  
 Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn Leu  
 325 330 335  
 Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu Asn  
 340 345 350  
 Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser  
 355 360 365  
 Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr  
 370 375 380

<210> 13  
<211> 444  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 13  
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ctggggcttg tgtgtcagaa gctgcctttg tcctctccat tcctccatcc ttgggcctgt 180  
ctggcctatg atgccctcat tcagctctca gggccagag gtgactggtg tggatcctgc 240  
tcgctgtgcc aagatggccc tccagatgcy gcataccatc cctcccctga tgcgggtgta 300  
gatgaggta tctcagatgg cataggtgag cagagtgtgg aggggtgaagc tatggttcaa 360  
cagcatttgg atggtgcctg aatccacatt cagttcctgt agccactgca ccaggccctg 420  
gtccgttgaa gaagcagtgg aggc 444

<210> 14  
<211> 4693  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 14  
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gccgcgggac tgctgcggga ggccggcagc gggggccgcg agcgggcgga ctggcggcgg 120  
cggcagctgc gaaaagtgcg gagtgtggag ctggaccagc tgccctgagca gccgctcttc 180  
cttgccgcct caccgcccgc ctctcagact tccccgtcgc cggagcccgc ggacgcagcg 240  
gggagtggga ccggcttcca gcctgtggcg gtgccgcgcg cccacggagc cgccagccgg 300  
cgccggcggc accttaccga gtcggtggcg gcggcgaca gcggcgctc gactcccgca 360  
gcggccgagc ccggggagaa gcgggcgccc gccgcgagc cgtctcctgc agcggccccc 420  
gccggtcgtg agatggagaa taaagaaact ctcaaagggt tgcacaagat ggatgatcgt 480  
ccagaggaac gaatgatcag ggagaaactg aaggcaacct gtatgccagc ctggaagcac 540  
gaatggttgg aaaggagaaa taggcgaggg cctgtggtgg taaaaccaat cccagttaaa 600  
ggagatggat ctgaaatgaa tcacttagca gctgagtctc caggagaggt ccaggcaagt 660  
gcggcttcac cagcttccaa aggccgacgc agtcttctc ctggcaactc cccatcaggt 720  
cgcacagtga aatcagaatc tccaggagta aggagaaaaa gactttcccc agtgcctttt 780  
cagatgggca gaatcacacc accccgaaga gcccttcac cagatggctt ctcaccatat 840  
agccctgagg aaacaaaccg ccgtgttaac aaagtgatgc gggccagact gtacttactg 900  
cagcagatag ggcctaactc tttcctgatt ggaggagaca gcccagacaa taaataccgg 960  
gtgtttattg ggcctcagaa ctgcagctgt gcacatggaa cattctgtat tcactgtcta 1020  
tttgtgatgc tccgggtgtt tcaactagaa ccttcagacc caatgttatg gagaaaaact 1080  
ttaaagaatt ttgaggttga gactttgttc cagaaatatc acagtaggcg tagctcaagg 1140  
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acattgtcat catctagtac ttctacatct agttcagaaa acagcataaa ggaatgaagag 1260  
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gaagacggct gcaggaacaa gctgcaccac cactgcatgt caatttgggc agaagagtgt 1380  
agaagaaata gagaaccttt aatatgtccc cttttagatg ctaagtggag atctcatgat 1440  
ttctacagcc acgagttgtc aagtcctgtg gattccccct cttccctcag agctgcacag 1500  
cagcaaaccg tacagcagca gcctttggct ggatcacgaa ggaatcaaga gagcaatttt 1560  
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agtggttctt cccagaccag tatctcagga gatgtggtgg aggcattgctg cagcgttctg 1860  
tcaatggtct gtgctgacct tgtctacaaa gtgtacgttg ctgctttaa aacattgaga 1920

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gccatgctgg tatatactcc ttgccacagt ttagcggaaa gaatcaaact tcagagactt 1980
ctccagccag ttgtagacac catcctagtc aaatgtgcag atgccaatag ccgcacaagt 2040
cagctgtcca tatcaacact gttggaactg tgcaaaggcc aagcaggaga gttggcagtt 2100
ggcagagaaa tactaaaagc tggatccatt ggtattggtg gtgttgatta tgtcttaaat 2160
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cttatagata gactgttggt ggaatttcct gctgaatttt atcctcatat tgcagtagt 2280
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tagtgcagaa act 4693

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&lt;210&gt; 15

&lt;211&gt; 1495

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 15

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1 5 10 15

Ala Arg Ala Ala Ala Gly Leu Leu Arg Glu Ala Gly Ser Gly Gly  
 20 25 30  
 Arg Glu Arg Ala Asp Trp Arg Arg Gln Leu Arg Lys Val Arg Ser  
 35 40 45  
 Val Glu Leu Asp Gln Leu Pro Glu Gln Pro Leu Phe Leu Ala Ala Ser  
 50 55 60  
 Pro Pro Ala Ser Ser Thr Ser Pro Ser Pro Glu Pro Ala Asp Ala Ala  
 65 70 75 80  
 Gly Ser Gly Thr Gly Phe Gln Pro Val Ala Val Pro Pro Pro His Gly  
 85 90 95  
 Ala Ala Ser Arg Arg Gly Ala His Leu Thr Glu Ser Val Ala Ala Pro  
 100 105 110  
 Asp Ser Gly Ala Ser Ser Pro Ala Ala Ala Glu Pro Gly Glu Lys Arg  
 115 120 125  
 Ala Pro Ala Ala Glu Pro Ser Pro Ala Ala Ala Pro Ala Gly Arg Glu  
 130 135 140  
 Met Glu Asn Lys Glu Thr Leu Lys Gly Leu His Lys Met Asp Asp Arg  
 145 150 155 160  
 Pro Glu Glu Arg Met Ile Arg Glu Lys Leu Lys Ala Thr Cys Met Pro  
 165 170 175  
 Ala Trp Lys His Glu Trp Leu Glu Arg Arg Asn Arg Arg Gly Pro Val  
 180 185 190  
 Val Val Lys Pro Ile Pro Val Lys Gly Asp Gly Ser Glu Met Asn His  
 195 200 205  
 Leu Ala Ala Glu Ser Pro Gly Glu Val Gln Ala Ser Ala Ala Ser Pro  
 210 215 220  
 Ala Ser Lys Gly Arg Arg Ser Pro Ser Pro Gly Asn Ser Pro Ser Gly  
 225 230 235 240  
 Arg Thr Val Lys Ser Glu Ser Pro Gly Val Arg Arg Lys Arg Val Ser  
 245 250 255  
 Pro Val Pro Phe Gln Ser Gly Arg Ile Thr Pro Pro Arg Arg Ala Pro  
 260 265 270  
 Ser Pro Asp Gly Phe Ser Pro Tyr Ser Pro Glu Glu Thr Asn Arg Arg  
 275 280 285  
 Val Asn Lys Val Met Arg Ala Arg Leu Tyr Leu Leu Gln Gln Ile Gly  
 290 295 300  
 Pro Asn Ser Phe Leu Ile Gly Gly Asp Ser Pro Asp Asn Lys Tyr Arg  
 305 310 315 320  
 Val Phe Ile Gly Pro Gln Asn Cys Ser Cys Ala His Gly Thr Phe Cys  
 325 330 335  
 Ile His Leu Leu Phe Val Met Leu Arg Val Phe Gln Leu Glu Pro Ser  
 340 345 350  
 Asp Pro Met Leu Trp Arg Lys Thr Leu Lys Asn Phe Glu Val Glu Ser  
 355 360 365  
 Leu Phe Gln Lys Tyr His Ser Arg Arg Ser Ser Arg Ile Lys Ala Pro  
 370 375 380  
 Ser Arg Asn Thr Ile Gln Lys Phe Val Ser Arg Met Ser Asn Ser His  
 385 390 395 400  
 Thr Leu Ser Ser Ser Ser Thr Ser Thr Ser Ser Ser Glu Asn Ser Ile  
 405 410 415  
 Lys Asp Glu Glu Glu Gln Met Cys Pro Ile Cys Leu Leu Gly Met Leu  
 420 425 430  
 Asp Glu Glu Ser Leu Thr Val Cys Glu Asp Gly Cys Arg Asn Lys Leu  
 435 440 445  
 His His His Cys Met Ser Ile Trp Ala Glu Glu Cys Arg Arg Asn Arg  
 450 455 460  
 Glu Pro Leu Ile Cys Pro Leu Cys Arg Ser Lys Trp Arg Ser His Asp  
 465 470 475 480  
 Phe Tyr Ser His Glu Leu Ser Ser Pro Val Asp Ser Pro Ser Ser Leu  
 485 490 495



Arg	Ala	Ala	Gln	Gln	Thr	Val	Gln	Gln	Pro	Leu	Ala	Gly	Ser	500	505	510		
Arg	Arg	Asn	Gln	Glu	Ser	Asn	Phe	Asn	Leu	Thr	His	Tyr	Gly	Thr	Gln	515	520	525
Gln	Ile	Pro	Pro	Ala	Tyr	Lys	Asp	Leu	Ala	Glu	Pro	Trp	Ile	Gln	Val	530	535	540
Phe	Gly	Met	Glu	Leu	Val	Gly	Cys	Leu	Phe	Ser	Arg	Asn	Trp	Asn	Val	545	550	555
Arg	Glu	Met	Ala	Leu	Arg	Arg	Leu	Ser	His	Asp	Val	Ser	Gly	Ala	Leu	565	570	575
Leu	Leu	Ala	Asn	Gly	Glu	Ser	Thr	Gly	Asn	Ser	Gly	Gly	Ser	Ser	Gly	580	585	590
Ser	Ser	Pro	Ser	Gly	Gly	Ala	Thr	Ser	Gly	Ser	Ser	Gln	Thr	Ser	Ile	595	600	605
Ser	Gly	Asp	Val	Val	Glu	Ala	Cys	Cys	Ser	Val	Leu	Ser	Met	Val	Cys	610	615	620
Ala	Asp	Pro	Val	Tyr	Lys	Val	Tyr	Val	Ala	Ala	Leu	Lys	Thr	Leu	Arg	625	630	635
Ala	Met	Leu	Val	Tyr	Thr	Pro	Cys	His	Ser	Leu	Ala	Glu	Arg	Ile	Lys	645	650	655
Leu	Gln	Arg	Leu	Leu	Gln	Pro	Val	Val	Asp	Thr	Ile	Leu	Val	Lys	Cys	660	665	670
Ala	Asp	Ala	Asn	Ser	Arg	Thr	Ser	Gln	Leu	Ser	Ile	Ser	Thr	Leu	Leu	675	680	685
Glu	Leu	Cys	Lys	Gly	Gln	Ala	Gly	Glu	Leu	Ala	Val	Gly	Arg	Glu	Ile	690	695	700
Leu	Lys	Ala	Gly	Ser	Ile	Gly	Ile	Gly	Gly	Val	Asp	Tyr	Val	Leu	Asn	705	710	715
Cys	Ile	Leu	Gly	Asn	Gln	Thr	Glu	Ser	Asn	Asn	Trp	Gln	Glu	Leu	Leu	725	730	735
Gly	Arg	Leu	Cys	Leu	Ile	Asp	Arg	Leu	Leu	Leu	Glu	Phe	Pro	Ala	Glu	740	745	750
Phe	Tyr	Pro	His	Ile	Val	Ser	Thr	Asp	Val	Ser	Gln	Ala	Glu	Pro	Val	755	760	765
Glu	Ile	Arg	Tyr	Lys	Lys	Leu	Leu	Ser	Leu	Leu	Thr	Phe	Ala	Leu	Gln	770	775	780
Ser	Ile	Asp	Asn	Ser	His	Ser	Met	Val	Gly	Lys	Leu	Ser	Arg	Arg	Ile	785	790	795
Tyr	Leu	Ser	Ser	Ala	Arg	Met	Val	Thr	Thr	Val	Pro	His	Val	Phe	Ser	805	810	815
Lys	Leu	Leu	Glu	Met	Leu	Ser	Val	Ser	Ser	Val	Ser	Thr	His	Phe	Thr	820	825	830
Arg	Met	Arg	Arg	Arg	Leu	Met	Ala	Tyr	Ala	Asp	Glu	Val	Glu	Ile	Ala	835	840	845
Glu	Ala	Ile	Gln	Leu	Gly	Val	Glu	Asp	Thr	Leu	Gln	Arg	Gln	Gln	His	850	855	860
Asn	Ser	Phe	Cys	Arg	His	Leu	Phe	Pro	Thr	Thr	Ile	Trp	Lys	Pro	Gln	865	870	875
Arg	Thr	Val	Pro	Leu	Glu	Cys	Thr	Val	His	Leu	Glu	Lys	Thr	Gly	Lys	885	890	895
Gly	Leu	Cys	Ala	Thr	Lys	Leu	Ser	Ala	Ser	Ser	Glu	Asp	Ile	Ser	Glu	900	905	910
Arg	Leu	Ala	Arg	Ile	Ser	Val	Gly	Pro	Ser	Ser	Ser	Thr	Thr	Thr	Thr	915	920	925
Thr	Thr	Thr	Thr	Glu	Gln	Pro	Lys	Pro	Met	Val	Gln	Thr	Lys	Gly	Arg	930	935	940
Pro	His	Ser	Gln	Cys	Leu	Asn	Ser	Ser	Pro	Leu	Ser	His	His	Ser	Gln	945	950	955
Leu	Met	Phe	Pro	Ala	Leu	Ser	Thr	Pro	Ser	Ser	Ser	Thr	Pro	Ser	Val	965	970	975

Pro Ala Gly Thr Ala Thr Asp Val Ser Lys His Arg Leu Gln Gly Phe  
 980 985 990  
 Ile Pro Cys Arg Ile Pro Ser Ala Ser Pro Gln Thr Gln Arg Lys Phe  
 995 1000 1005  
 Ser Leu Gln Phe His Arg Asn Cys Pro Glu Asn Lys Asp Ser Asp Lys  
 1010 1015 1020  
 Leu Ser Pro Val Phe Thr Gln Ser Arg Pro Leu Pro Ser Ser Asn Ile  
 1025 1030 1035 1040  
 His Arg Pro Lys Pro Ser Arg Pro Thr Pro Gly Asn Thr Ser Lys Gln  
 1045 1050 1055  
 Gly Asp Pro Ser Lys Asn Ser Met Thr Leu Asp Leu Asn Ser Ser Ser  
 1060 1065 1070  
 Lys Cys Asp Asp Ser Phe Gly Leu Ser Ser Asn Ser Ser Asn Cys Cys  
 1075 1080 1085  
 Tyr Thr Ser Asp Glu Thr Val Phe Thr Pro Val Glu Glu Lys Cys Arg  
 1090 1095 1100  
 Leu Asp Val Asn Thr Glu Leu Asn Ser Ser Ile Glu Asp Leu Leu Glu  
 1105 1110 1115 1120  
 Ala Ser Met Pro Ser Ser Asp Thr Thr Val Thr Phe Lys Ser Glu Val  
 1125 1130 1135  
 Ala Val Leu Ser Pro Glu Lys Ala Glu Asn Asp Asp Thr Tyr Lys Asp  
 1140 1145 1150  
 Asp Val Asn His Asn Gln Lys Cys Lys Glu Lys Met Glu Ala Glu Glu  
 1155 1160 1165  
 Glu Glu Ala Leu Ala Ile Ala Met Ala Met Ser Ala Ser Gln Val Ala  
 1170 1175 1180  
 Leu Pro Ile Val Pro Gln Leu Gln Val Glu Asn Gly Glu Asp Ile Ile  
 1185 1190 1195 1200  
 Ile Ile Gln Gln Asp Thr Pro Glu Thr Leu Pro Gly His Thr Lys Ala  
 1205 1210 1215  
 Lys Gln Pro Tyr Arg Glu Asp Thr Glu Trp Leu Lys Gly Gln Gln Ile  
 1220 1225 1230  
 Gly Leu Gly Ala Phe Ser Ser Cys Tyr Gln Ala Gln Asp Val Gly Thr  
 1235 1240 1245  
 Gly Thr Leu Met Ala Val Lys Gln Val Thr Tyr Val Arg Asn Thr Ser  
 1250 1255 1260  
 Ser Glu Gln Glu Glu Val Val Glu Ala Leu Arg Glu Glu Ile Arg Met  
 1265 1270 1275 1280  
 Met Ser His Leu Asn His Pro Asn Ile Ile Arg Met Leu Gly Ala Thr  
 1285 1290 1295  
 Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile Glu Trp Met Ala Gly Gly  
 1300 1305 1310  
 Ser Val Ala His Leu Leu Ser Lys Tyr Gly Ala Phe Lys Glu Ser Val  
 1315 1320 1325  
 Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg Gly Leu Ser Tyr Leu His  
 1330 1335 1340  
 Glu Asn Gln Ile Ile His Arg Asp Val Lys Gly Ala Asn Leu Leu Ile  
 1345 1350 1355 1360  
 Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala Asp Phe Gly Ala Ala Ala  
 1365 1370 1375  
 Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly Glu Phe Gln Gly Gln Leu  
 1380 1385 1390  
 Leu Gly Thr Ile Ala Phe Met Ala Pro Glu Val Leu Arg Gly Gln Gln  
 1395 1400 1405  
 Tyr Gly Arg Ser Cys Asp Val Trp Ser Val Gly Cys Ala Ile Ile Glu  
 1410 1415 1420  
 Met Ala Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys His Ser Asn His  
 1425 1430 1435 1440  
 Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile  
 1445 1450 1455

Pro Ser His Leu Ser Pro Gly Leu Arg Asp Val Ala Leu Arg Cys Leu  
 1460 1465 1470  
 Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu Leu Leu Lys His  
 1475 1480 1485  
 Pro Val Phe Arg Thr Thr Trp  
 1490 1495

&lt;210&gt; 16

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

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tgggggtcact cttaacgcag tgtaaaaggt aagccct

37

&lt;210&gt; 17

&lt;211&gt; 2348

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 17

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atctggtggc	cctccagatg	aaccgacgtc	accggatgcc	tggatatgag	accatgaaga	180
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gggagagggc	aattatagcg	ttcagccggc	ctgtgaaata	tgaagatgtg	gagcacaagg	300
tgacaacagt	atttggacaa	cctcttgatc	tacattacat	gaacaatgag	ctctccatcc	360
tgctgaaaaa	ccaagatgat	cttgataaag	caattgacat	tttagataga	agctcaagca	420
tgaaaagcct	taggatattg	ctgttgctcc	aggacagaaa	ccataacagt	tcctctcccc	480
actctgaggt	gtccagacag	gtgcggtatc	aggcttccca	gtccgcaggg	gatataaata	540
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tcggcagggg	ctatttgtgc	tatgacgtgg	acacgggacg	tgaacttgct	tccaagcagg	1260
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ttggccgcat	cttcaagatt	gccaccagc	ccaccaatcc	tcagctgccc	tcccacatct	1860
ctgaacatgg	ccgggacttc	ctgaggcgca	tttttgtgga	ggctcgccag	agaccttcag	1920

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ctgaggagct gctcacacac cactttgcac agctcatgta ctgagctctc acggccacac 1980
agctgccggt cgccctttgc tgcattggcag ggggctgctg ctgggctcag tgaagttgct 2040
gcttctccca ggcaaggctg tggaccatgg agtggcagcc cagccagcgt cggctctgtgc 2100
cccttccgcc actggggctc agagccgggg tgggggtggct gcagcctcag gactggggagc 2160
ccccagcctg tcagatccag gagctccagt gtccctgagct cagcgtggag gggtaggggc 2220
tgggaacagt gtgcaaggca gccgtggggc ccaccctcgg ggatgtgtcc tgacactgca 2280
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ttattttc 2348

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&lt;210&gt; 18

&lt;211&gt; 626

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 18

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Met Asp Glu Gln Glu Ala Leu Asn Ser Ile Met Asn Asp Leu Val Ala
1      5      10      15
Leu Gln Met Asn Arg Arg His Arg Met Pro Gly Tyr Glu Thr Met Lys
20     25     30
Asn Lys Asp Thr Gly His Ser Asn Arg Gln Ser Asp Val Arg Ile Lys
35     40     45
Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val
50     55     60
Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro
65     70     75     80
Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn
85     90     95
Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser
100    105    110
Met Lys Ser Leu Arg Ile Leu Leu Ser Gln Asp Arg Asn His Asn
115    120    125
Ser Ser Ser Pro His Ser Glu Val Ser Arg Gln Val Arg Ile Lys Ala
130    135    140
Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro
145    150    155    160
Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser
165    170    175
Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln
180    185    190
Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr
195    200    205
Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu
210    215    220
Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe
225    230    235    240
Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln
245    250    255
Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly
260    265    270
Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr
275    280    285
Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn
290    295    300
Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu
305    310    315    320
Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg
325    330    335

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Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro  
 340 345 350  
 Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu  
 355 360 365  
 Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr  
 370 375 380  
 Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro  
 385 390 395 400  
 Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu  
 405 410 415  
 Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg  
 420 425 430  
 Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly  
 435 440 445  
 Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser  
 450 455 460  
 Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu  
 465 470 475 480  
 His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu  
 485 490 495  
 Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys  
 500 505 510  
 Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr  
 515 520 525  
 Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr  
 530 535 540  
 Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met  
 545 550 555 560  
 Leu Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile  
 565 570 575  
 Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile  
 580 585 590  
 Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg  
 595 600 605  
 Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu  
 610 615 620  
 Met Tyr  
 625

&lt;210&gt; 19

&lt;211&gt; 1576

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 19

gaattcgagc	cgaccgaccg	ctcccggccc	gccccctatg	ggccccgggt	agaggcgccg	60
ccgcccggcg	cccgcggagc	cccgatgctg	gcccggagga	agccggtgct	gccggcgctc	120
accatcaacc	ctaccatcgc	cgaggggcca	tcccctacca	gcgagggcgc	ctccgaggca	180
aacctggtgg	acctgcagaa	gaagctggag	gagctggaac	ttgacgagca	gcagaagaag	240
cggttggaag	cctttctcac	ccagaaagcc	aaggttggcg	aactcaaaga	cgatgacttc	300
gaaaggatct	cagagctggg	cgcgggcaac	ggcgggggtg	tcaccaaagt	ccagcacaga	360
ccctcggggc	tcatcatggc	caggaagctg	atccaccttg	agatcaagcc	ggccatccgg	420
aaccagatca	tccgcgagct	gcaggtcctg	cacgaatgca	actcgccgta	catcgtgggc	480
ttctacgggg	cctttctacag	tgacggggag	atcagcattt	gcatggaaca	catggacggc	540
ggctccctgg	accaggtgct	gaaagaggcc	aagaggattc	ccgaggagat	cctggggaaa	600
gtcagcatcg	cggttctccg	gggcttggcg	tacctccgag	agaagcacca	gatcatgcac	660

cgagatgtga	agccctccaa	catcctcgtg	aactctagag	gggagatcaa	gctgtgtgac	720
ttcgggggtga	gcgccagct	catagactcc	atggccaact	ccttcgtggg	cacgcgctcc	780
tacatggctc	cggagcgggt	gcagggcaca	cattactcgg	tgcagtcgga	catctggagc	840
atgggcctgt	ccctggtgga	gctggccgtc	ggaagggtacc	ccatccccc	gcccgaagcc	900
aaagagctgg	aggccatctt	tggccggccc	gtggctcgacg	gggaagaagg	agagcctcac	960
agcatctcgc	ctcggccgag	gccccccggg	cgccccgtca	gcggtcacgg	gatggatagc	1020
cggcctgcca	tggccatctt	tgaactcctg	gactatattg	tgaacgagcc	acctcctaag	1080
ctgccccaacg	gtgtgttcac	ccccgacttc	caggagtttg	tcaataaatg	cctcatcaag	1140
aaccagcgg	agcgggcgga	cctgaagatg	ctcacaaaacc	acaccttcat	caagcggctcc	1200
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ggcacacca	cgcgcaccgc	cgtgtgacag	tggccgggct	ccctgcgtcc	cgtggtgac	1320
ctgcccaccg	tccctgtcca	tgccccgccc	ttccagctga	ggacacgtgg	cgcctccacc	1380
caccctcctg	cctcacctcg	cggagagcac	cgtggcgggg	cgacagcgca	tgcaggaacg	1440
ggggtctcct	ctcctgccag	tcctggccgg	ggtgcctctg	gggacgggcg	acgctgctgt	1500
gtgtggtctc	agaggctctg	cttccttagg	ttacaaaaca	aaacagggag	agaaaagcaa	1560
aaaaaaaaaa	aaaaaa					1576

&lt;210&gt; 20

&lt;211&gt; 2222

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 20

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cccgggtcca	aaatgcccac	gaagaagccg	acgcccatac	agctgaaccc	ggcccccgac	120
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aagcagaagg	tgggagaact	gaaggatgac	gactttgaga	agatcagtga	gctggggggt	300
ggcaatggcg	gtgtggtggt	caagggtctc	cacaagcctt	ctggcctggg	catggccaga	360
aagctaattc	atctggagat	caaaccgcga	atccgggaac	agatcataag	ggagctgcag	420
gttctgcatc	agtgaactc	tccgtacatc	gtgggcttct	atggtgcgtt	ctacagcgat	480
ggcgagatca	gtatctgcat	ggagcacatg	gatggagggt	ctctggatca	agtcctgaag	540
aaagctggaa	gaattcctga	acaaatttta	ggaaaagtta	gcattgctgt	aataaaaggc	600
ctgacataatc	tgaggggagaa	gcacaagatc	atgcacagag	atgtcaagcc	ctccaacatc	660
ctagtcaact	cccgtgggga	gatcaagctc	tgtgactttg	gggtcagcgg	gcagctcatc	720
gactccatgg	ccaactcctt	cgtgggcaca	aggtcctaca	tgtcgccaga	aagactccag	780
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cttagctcat	acggaatgga	cagccgacct	cccatggcaa	tttttgagtt	gttggattac	1020
atagtcaacg	agcctcctcc	aaaactgccc	agtggagtgt	tcagtctgga	atttcaagat	1080
tttgtgaata	aatgcttaat	aaaaaacccc	gcagagagag	cagatttgaa	gcaactcatg	1140
gttcatgctt	ttatcaagag	atctgatgct	gaggaagtgg	atattgcagg	ttggctctgc	1200
tccaccatcg	gccttaacca	gcccagcaca	ccaaccatg	ctgctggcgt	ctaagtgttt	1260
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gcattgtgcca	agattctact	cttgtcattt	ttaattattc	tgtctttatt	cttattacta	1440
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tcaaaacctg	tgccaggctg	aattacagtg	aaatttttgg	tgaatgtggg	tagtcattct	1560
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aataaaaaaa	aaaggagaaa	gctaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2220
aa						2222

&lt;210&gt; 21

&lt;211&gt; 2371

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 21

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agagtgggaat	gatccccgag	gcccaggggc	tcgtgcttcc	gcagtagtca	gtccccgtga	240
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gagcaggcaa	atgtgcaata	ccaacatgtc	tgtacctact	gatgggtgctg	taaccacctc	360
acagattcca	gcttcggaac	aagagaccct	ggtagacca	aagccattgc	ttttgaagtt	420
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tggccagtat	attatgacta	aacgattata	tgatgagaag	caacaacata	ttgtatattg	540
ttcaaatgat	cttctaggag	atthgtttgg	cgtgccaaagc	ttctctgtga	aagagcacag	600
gaaaatatat	accatgatct	acaggaactt	ggtagtagtc	aatcagcagg	aatcatcgga	660
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ggctctgtgt	gtaataaggg	agatatgttg	tgaaagaagc	agtagcagtg	aatctacagg	960
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atcaacttct	agtagcatta	tttatagcag	ccaagaagat	gtgaaagagt	ttgaaaggga	1560
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acatatatca	aagtgagaaa	atgcctcaat	tcacatagat	ttcttctctt	tagtataatt	1920
gacctacttt	ggtagtgga	tagtgaatac	ttactataat	ttgacttgaa	tatgtagctc	1980
atccttttaca	ccaactccta	atthtaata	atthtactc	tgtcttaaat	gagaagtact	2040
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ccgtgttagc	caggatgggc	tcgatctcct	gacctcgtga	tccgcccacc	tcggcctccc	2340
aaagtgtctg	gattacaggc	atgagccacc	g			2371

&lt;210&gt; 22

&lt;211&gt; 491

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 22

Met	Cys	Asn	Thr	Asn	Met	Ser	Val	Pro	Thr	Asp	Gly	Ala	Val	Thr	Thr
1				5				10						15	
Ser	Gln	Ile	Pro	Ala	Ser	Glu	Gln	Glu	Thr	Leu	Val	Arg	Pro	Lys	Pro
		20					25						30		
Leu	Leu	Leu	Lys	Leu	Leu	Lys	Ser	Val	Gly	Ala	Gln	Lys	Asp	Thr	Tyr
		35					40					45			
Thr	Met	Lys	Glu	Val	Leu	Phe	Tyr	Leu	Gly	Gln	Tyr	Ile	Met	Thr	Lys
	50					55					60				
Arg	Leu	Tyr	Asp	Glu	Lys	Gln	Gln	His	Ile	Val	Tyr	Cys	Ser	Asn	Asp
65					70					75				80	
Leu	Leu	Gly	Asp	Leu	Phe	Gly	Val	Pro	Ser	Phe	Ser	Val	Lys	Glu	His
			85					90						95	
Arg	Lys	Ile	Tyr	Thr	Met	Ile	Tyr	Arg	Asn	Leu	Val	Val	Val	Asn	Gln
		100						105						110	
Gln	Glu	Ser	Ser	Asp	Ser	Gly	Thr	Ser	Val	Ser	Glu	Asn	Arg	Cys	His
		115				120						125			
Leu	Glu	Gly	Gly	Ser	Asp	Gln	Lys	Asp	Leu	Val	Gln	Glu	Leu	Gln	Glu
	130					135					140				
Glu	Lys	Pro	Ser	Ser	Ser	His	Leu	Val	Ser	Arg	Pro	Ser	Thr	Ser	Ser
145					150					155				160	
Arg	Arg	Arg	Ala	Ile	Ser	Glu	Thr	Glu	Glu	Asn	Ser	Asp	Glu	Leu	Ser
			165					170						175	
Gly	Glu	Arg	Gln	Arg	Lys	Arg	His	Lys	Ser	Asp	Ser	Ile	Ser	Leu	Ser
		180						185					190		
Phe	Asp	Glu	Ser	Leu	Ala	Leu	Cys	Val	Ile	Arg	Glu	Ile	Cys	Cys	Glu
	195					200						205			
Arg	Ser	Ser	Ser	Ser	Glu	Ser	Thr	Gly	Thr	Pro	Ser	Asn	Pro	Asp	Leu
	210				215					220					
Asp	Ala	Gly	Val	Ser	Glu	His	Ser	Gly	Asp	Trp	Leu	Asp	Gln	Asp	Ser
225				230					235					240	
Val	Ser	Asp	Gln	Phe	Ser	Val	Glu	Phe	Glu	Val	Glu	Ser	Leu	Asp	Ser
			245					250					255		
Glu	Asp	Tyr	Ser	Leu	Ser	Glu	Glu	Gly	Gln	Glu	Leu	Ser	Asp	Glu	Asp
		260						265					270		
Asp	Glu	Val	Tyr	Gln	Val	Thr	Val	Tyr	Gln	Ala	Gly	Glu	Ser	Asp	Thr
	275					280						285			
Asp	Ser	Phe	Glu	Glu	Asp	Pro	Glu	Ile	Ser	Leu	Ala	Asp	Tyr	Trp	Lys
	290				295					300					
Cys	Thr	Ser	Cys	Asn	Glu	Met	Asn	Pro	Pro	Leu	Pro	Ser	His	Cys	Asn
305				310						315				320	
Arg	Cys	Trp	Ala	Leu	Arg	Glu	Asn	Trp	Leu	Pro	Glu	Asp	Lys	Gly	Lys
			325					330						335	
Asp	Lys	Gly	Glu	Ile	Ser	Glu	Lys	Ala	Lys	Leu	Glu	Asn	Ser	Thr	Gln
		340						345					350		
Ala	Glu	Glu	Gly	Phe	Asp	Val	Pro	Asp	Cys	Lys	Lys	Thr	Ile	Val	Asn
	355					360						365			
Asp	Ser	Arg	Glu	Ser	Cys	Val	Glu	Glu	Asn	Asp	Asp	Lys	Ile	Thr	Gln
	370				375					380					
Ala	Ser	Gln	Ser	Gln	Glu	Ser	Glu	Asp	Tyr	Ser	Gln	Pro	Ser	Thr	Ser
385				390					395					400	
Ser	Ser	Ile	Ile	Tyr	Ser	Ser	Gln	Glu	Asp	Val	Lys	Glu	Phe	Glu	Arg
			405					410						415	
Glu	Glu	Thr	Gln	Asp	Lys	Glu	Glu	Ser	Val	Glu	Ser	Ser	Leu	Pro	Leu
		420						425					430		



Asn Ala Ile Glu Pro Cys Val Ile Cys Gln Gly Arg Pro Lys Asn Gly  
 435 440 445  
 Cys Ile Val His Gly Lys Thr Gly His Leu Met Ala Cys Phe Thr Cys  
 450 455 460  
 Ala Lys Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val Cys Arg Gln  
 465 470 475 480  
 Pro Ile Gln Met Ile Val Leu Thr Tyr Phe Pro  
 485 490

&lt;210&gt; 23

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 23

```

gagactgtgc cctgtccacg gtgcctcctg catgtcctgc tgccctgagc tgtcccagagc      60
taggtgacag cgtaccacgc tgccaccatg aatgaggtgt ctgtcatcaa agaaggctgg      120
ctccacaagc gtggtgaata catcaagacc tggaggccac ggtacttcct gctgaagagc      180
gacggctcct tcattgggta caaggagagg cccgaggccc ctgatcagac tctacccccc      240
ttaaacaact tctccgtagc agaatgccag ctgatgaaga ccgagaggcc gcgacccaac      300
acctttgtca tacgtgcctt gcagtggacc acagtcacgc agaggacctt ccacgtggat      360
tctccagacg agagggagga gtggatgcgg gccatccaga tggtcgcca cagcctcaag      420
cagcggggccc caggcgagga ccccatggac tacaagtgtg gctccccag tgactcctcc      480
acgactgagg agatggaagt ggcgggtcagc aaggcacggg ctaaagtgc catgaatgac      540
ttcgactatc tcaaaactcct tggcaaggga acctttggca aagtcacctt ggtgcgggag      600
aaggccactg gccgtacta cgccatgaag atcctgcgaa aggaagtcac cattgccaag      660
gatgaagtcg ctacacacag caccgagagc cgggtcctcc agaacaccag gcacccgttc      720
ctcactgcgc tgaagtatgc cttccagacc cagaccgcc tgtgctttgt gatggagtat      780
gccaacgggg gtgagctgtt cttccacctg tcccgggagc gtgtcttcac agaggagcgg      840
gcccggtttt atggtgcaga gattgtctcg gctcttgagt acttgactc gcgggacgtg      900
gtataccgcg acatcaagct ggaaaacctc atgctggaca aagatggcca catcaagatc      960
actgactttg gcctctgcaa agagggcatc agtgacgggg ccaccatgaa aaccttctgt      1020
gggaccccg agtacctggc gcctgaggtg ctggaggaca atgactatgg ccgggcccgtg      1080
gactggtggg ggctgggtgt ggtcatgtac gagatgatgt gcggccgcct gcccttctac      1140
aaccaggacc acgagcgcct cttcgagctc atcctcatgg aagagatccg cttcccgcgc      1200
acgctcagcc ccgaggccaa gtccctgctt gctgggctgc ttaagaagga cccaagcag      1260
aggcttggtg gggggcccag cgatgccaa gaggatcatg agcacaggtt cttcctcagc      1320
atcaactggc aggacgtggt ccagaagaag ctccctgccac cttcaaacc tcaggtcacg      1380
tccgaggtcg acacaaggta cttcgatgat gaatttaccg cccagtccat cacaatcaca      1440
ccccctgacc gctatgacag cctgggctta ctggagctgg accagcggac ccacttcccc      1500
cagttctcct actcggccag catccgcgag tgagcagctt gccacgcag aggcgcgacg      1560
ctcgctgcca tcaccgctgg gtggtttttt acccctgcc      1599

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&lt;210&gt; 24

&lt;211&gt; 481

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 24

Met Asn Glu Val Ser Val Ile Lys Glu Gly Trp Leu His Lys Arg Gly  
 1 5 10 15  
 Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Ser Asp  
 20 25 30

Gly Ser Phe Ile Gly Tyr Lys Glu Arg Pro Glu Ala Pro Asp Gln Thr  
 35 40 45  
 Leu Pro Pro Leu Asn Asn Phe Ser Val Ala Glu Cys Gln Leu Met Lys  
 50 55 60  
 Thr Glu Arg Pro Arg Pro Asn Thr Phe Val Ile Arg Cys Leu Gln Trp  
 65 70 75 80  
 Thr Thr Val Ile Glu Arg Thr Phe His Val Asp Ser Pro Asp Glu Arg  
 85 90 95  
 Glu Glu Trp Met Arg Ala Ile Gln Met Val Ala Asn Ser Leu Lys Gln  
 100 105 110  
 Arg Ala Pro Gly Glu Asp Pro Met Asp Tyr Lys Cys Gly Ser Pro Ser  
 115 120 125  
 Asp Ser Ser Thr Thr Glu Glu Met Glu Val Ala Val Ser Lys Ala Arg  
 130 135 140  
 Ala Lys Val Thr Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys  
 145 150 155 160  
 Gly Thr Phe Gly Lys Val Ile Leu Val Arg Glu Lys Ala Thr Gly Arg  
 165 170 175  
 Tyr Tyr Ala Met Lys Ile Leu Arg Lys Glu Val Ile Ile Ala Lys Asp  
 180 185 190  
 Glu Val Ala His Thr Val Thr Glu Ser Arg Val Leu Gln Asn Thr Arg  
 195 200 205  
 His Pro Phe Leu Thr Ala Leu Lys Tyr Ala Phe Gln Thr His Asp Arg  
 210 215 220  
 Leu Cys Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His  
 225 230 235 240  
 Leu Ser Arg Glu Arg Val Phe Thr Glu Glu Arg Ala Arg Phe Tyr Gly  
 245 250 255  
 Ala Glu Ile Val Ser Ala Leu Glu Tyr Leu His Ser Arg Asp Val Val  
 260 265 270  
 Tyr Arg Asp Ile Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His  
 275 280 285  
 Ile Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Ser Asp Gly  
 290 295 300  
 Ala Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu  
 305 310 315 320  
 Val Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu  
 325 330 335  
 Gly Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn  
 340 345 350  
 Gln Asp His Glu Arg Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg  
 355 360 365  
 Phe Pro Arg Thr Leu Ser Pro Glu Ala Lys Ser Leu Leu Ala Gly Leu  
 370 375 380  
 Leu Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Pro Ser Asp Ala  
 385 390 395 400  
 Lys Glu Val Met Glu His Arg Phe Phe Leu Ser Ile Asn Trp Gln Asp  
 405 410 415  
 Val Val Gln Lys Lys Leu Leu Pro Pro Phe Lys Pro Gln Val Thr Ser  
 420 425 430  
 Glu Val Asp Thr Arg Tyr Phe Asp Glu Phe Thr Ala Gln Ser Ile  
 435 440 445  
 Thr Ile Thr Pro Pro Asp Arg Tyr Asp Ser Leu Gly Leu Leu Glu Leu  
 450 455 460  
 Asp Gln Arg Thr His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ile Arg  
 465 470 475 480  
 Glu

&lt;210&gt; 25

&lt;211&gt; 1547

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 25

```

gggagtcattc atgagcgcgtg ttaccattgt gaaagaagggt tgggttcaga agagggggaga      60
atatataaaa aactggagggc caagatactt ccttttgaag acagatgggt cattcatagg      120
atataaagag aaacctcaag atgtggattt accttatccc ctcaacaact tttcagtggc      180
aaaatgccag ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct      240
ccagtggact actgttatag agagaacatt tcatgtagat actccagagg aaaggggaaga      300
atggacagaa gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat      360
gaattgtagt ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac      420
aaccatcat aaaagaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg      480
cacttttggg aaagtatttt tggttcgaga gaaggcaagt ggaaaatact atgctatgaa      540
gattctgaag aaagaagtca ttattgcaa ggatgaagtg gcacacactc taactgaaa      600
cagagtatta aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttccagac      660
aaaagaccgt ttgtgttttg tgatggaata tgtaaatggg ggcgagctgt ttttccattt      720
gtcgagagag cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc      780
tgccttggac tatctacatt cgggaaagat tgtgtaccgt gatctcaagt tggagaatct      840
aatgctggac aaagatggcc acataaaaat tacagatttt ggactttgca aagaagggat      900
cacagatgca gccaccatga agacattctg tggcactcca gaatatctgg caccagaggt      960
gttagaagat aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta      1020
tgaaatgatg tgtgggagggt tacctttcta caaccaggac catgagaaac tttttgaatt      1080
aatattaatg gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct      1140
ttcagggctc ttgataaagg atccaaataa acgccttggt ggaggaccag atgatgcaaa      1200
agaaattatg agacacagtt tcttctctgg agtaactgg caagatgtat atgataaaaa      1260
gcttctaact ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga      1320
agaatttaca gctcagacta ttacaataac accacctgaa aaatatgatg aggatggtat      1380
ggactgcatg gacaatgaga ggcggccgca tttccctcaa ttttctact ctgcaagtgg      1440
acgagaataa gtctctttca ttctgtact tcactgtcat cttcaattta ttactgaaaa      1500
tgattcctgg acatcaccag tcctagctct tacacatagc aggggca      1547

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&lt;210&gt; 26

&lt;211&gt; 479

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 26

```

Met Ser Asp Val Thr Ile Val Lys Glu Gly Trp Val Gln Lys Arg Gly
 1           5           10          15
Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp
          20          25          30
Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
          35          40          45
Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
          50          55          60
Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
          65          70          75          80
Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
          85          90          95
Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
          100         105         110
Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
          115         120         125

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Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr  
 130 135 140  
 Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly  
 145 150 155 160  
 Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met  
 165 170 175  
 Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His  
 180 185 190  
 Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu  
 195 200 205  
 Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val  
 210 215 220  
 Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu  
 225 230 235 240  
 Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val  
 245 250 255  
 Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu  
 260 265 270  
 Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr  
 275 280 285  
 Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys  
 290 295 300  
 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp  
 305 310 315 320  
 Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met  
 325 330 335  
 Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu  
 340 345 350  
 Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr  
 355 360 365  
 Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp  
 370 375 380  
 Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met  
 385 390 395 400  
 Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys  
 405 410 415  
 Lys Leu Val Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr  
 420 425 430  
 Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro  
 435 440 445  
 Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg  
 450 455 460  
 Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu  
 465 470 475

&lt;210&gt; 27

&lt;211&gt; 2277

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 27

ctctgggggt gctgctgagc gaggcgagag gcagcctcct cctctcggcc agaggcagga	60
gcgaggcgag cgcggggaag gcaggccggc agcccgtgtg agcccatgc ggcgagcgcc	120
tgcgagaagg ggaggaggag ccggcccgcc gcccgccgcc cggggatggt gaggaggcgg	180
cgctgcgtga gcccagttag gccttcgctc gggcccgccg ccagctctcc ctctctccgc	240
tcgctcgctc ccccttccc tctccttccc tgccgcgcgc gccgcgcgcc tcccatcacc	300
tcctccccgg gctcccgcag ccataagtag ctgagaagga gaaagacaag aaaaagaaca	360

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tcccttttgt ggacccttct gctggagttc aggaatttca acggtgatct tttgactgat 420
ccaccagcct gataaactga tccaccaaga gacattcccc ccattatgaa tgaagtagcg 480
atagtgaagg aaggatggct ccacaaacga ggagaatata tcaaaacatg gaggccacgg 540
tattttcttt taaagaatga tggcacattc attggctaca aggaacgacc gcaagacgtt 600
gaccaacgag aatcaccttt aaataacttc tcagtagctc agtgccagct gatgaagaca 660
gaacgaccta aaccaaacac atttatcatt agatgcctcc agtggaccac agtaattgaa 720
agaacatttc atgtggagac tccagaggag cgggaagaat ggacaaaagc tatccaaact 780
gttgcgagaca gcctcaagaa acaggaggaa gagatgatgg atttttagatc tggttctcct 840
agtgataatt caggtgctga agaaatggaa gtttctatga caaagccaaa acacaaagt 900
accatgaatg aatttgaata ccttaagcta ctgggaaaag gcacttttgg aaagggtcatt 960
ttagttaaag aaaaagcaac cggacgggat tatgctatga aaattctgaa gaaggaagtt 1020
attgtagcaa aggatgaagt agcacacacg ctgacagaaa accgtgtttt acagaactca 1080
cggcatccat tcttaacagc tttaaagtat tcccttcaga cacacgatcg cttgtgtttt 1140
gttatggagt atgctaacgg aggggagttg tttttccatc tgtcgagaga gcgtgtattt 1200
tctgaagacc gggcgctgtt ttatggggct gagattgttt cagcgctgga ttacctgcat 1260
tcagagaaga atgtggtgta cagagatttg aagctggaaa atcttatgct ggataaagac 1320
gggcacataa aaattacaga ctttggacta tgtaaagaag gcataaaaga tggagcaaca 1380
atgaagactt tctgtggcac tccagagtat cttgcaccag aggtgctgga ggataatgac 1440
tatggtcgtg cagtggactg gtggggatta ggagttgtga tgtatgaaat gatgtgtggc 1500
cggctcccct tctacaatca ggaccatgaa aagctctttg aactcatcct tatggaagag 1560
attagatttc cagcactttt gtcacctgaa gcaaaatctc tcttgtcagg tttgctgaag 1620
aaagatccta agcaaagggt agggggcggg cctgatgatg ccaaggagat tatgcagcac 1680
aaattctttg ctggcattgt ttggcaagat gtatacggga agaagcttgt acctccattt 1740
aagccacaag ttacatctga aacagatata agatactttg atgaagaatt tacagcacag 1800
atgattacaa tcaactcctc tgaccaagat gacagcatgg attgtgtaga caatgagaga 1860
agacctcatt ttcctcagtt ctctatttca gccagtggaa ccgcttaatg ttttgcatg 1920
ttttcccatc cagaaacaaa acagactgca ttttggggac cttacttcaa tggacactag 1980
agaactttct atattatctg aattacaacac tgtgtttgta ttacgattta gatgaatttc 2040
taggaagcct cacagattct gtatttaaaa caattctttg atgcattttt gagaaggaaa 2100
acaaatccat tcttaaagta ttacgtcaag gctcttatgc tgaacgacca taggttttta 2160
agaatatgca ccaaaactgt ttactttaga attaattaag gcattcaata tcagctatag 2220
gatctaatac ttcctgtcaa aagttaaga ccaggaacct tagagtagaa acgaaac 2277

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&lt;210&gt; 28

&lt;211&gt; 480

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 28

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Met Asn Glu Val Ala Ile Val Lys Glu Gly Trp Leu His Lys Arg Gly
1           5           10          15
Glu Tyr Ile Lys Thr Trp Arg Pro Arg Tyr Phe Leu Leu Lys Asn Asp
20          25          30
Gly Thr Phe Ile Gly Tyr Lys Glu Arg Pro Gln Asp Val Asp Gln Arg
35          40          45
Glu Ser Pro Leu Asn Asn Phe Ser Val Ala Gln Cys Gln Leu Met Lys
50          55          60
Thr Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp
65          70          75          80
Thr Thr Val Ile Glu Arg Thr Phe His Val Glu Thr Pro Glu Glu Arg
85          90          95
Glu Glu Trp Thr Lys Ala Ile Gln Thr Val Ala Asp Ser Leu Lys Lys
100         105         110
Gln Glu Glu Glu Met Met Asp Phe Arg Ser Gly Ser Pro Ser Asp Asn
115         120         125
Ser Gly Ala Glu Glu Met Glu Val Ser Met Thr Lys Pro Lys His Lys
130         135         140

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Val Thr Met Asn Glu Phe Glu Tyr Leu Lys Leu Leu Gly Lys Gly Thr  
 145 150 155 160  
 Phe Gly Lys Val Ile Leu Val Lys Glu Lys Ala Thr Gly Arg Tyr Tyr  
 165 170 175  
 Ala Met Lys Ile Leu Lys Lys Glu Val Ile Val Ala Lys Asp Glu Val  
 180 185 190  
 Ala His Thr Leu Thr Glu Asn Arg Val Leu Gln Asn Ser Arg His Pro  
 195 200 205  
 Phe Leu Thr Ala Leu Lys Tyr Ser Phe Gln Thr His Asp Arg Leu Cys  
 210 215 220  
 Phe Val Met Glu Tyr Ala Asn Gly Gly Glu Leu Phe Phe His Leu Ser  
 225 230 235 240  
 Arg Glu Arg Val Phe Ser Glu Asp Arg Ala Arg Phe Tyr Gly Ala Glu  
 245 250 255  
 Ile Val Ser Ala Leu Asp Tyr Leu His Ser Glu Lys Asn Val Val Tyr  
 260 265 270  
 Arg Asp Leu Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile  
 275 280 285  
 Lys Ile Thr Asp Phe Gly Leu Cys Lys Glu Gly Ile Lys Asp Gly Ala  
 290 295 300  
 Thr Met Lys Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val  
 305 310 315 320  
 Leu Glu Asp Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly  
 325 330 335  
 Val Val Met Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln  
 340 345 350  
 Asp His Glu Lys Leu Phe Glu Leu Ile Leu Met Glu Glu Ile Arg Phe  
 355 360 365  
 Pro Arg Thr Leu Ser Pro Glu Ala Lys Ser Leu Leu Ser Gly Leu Leu  
 370 375 380  
 Lys Lys Asp Pro Lys Gln Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys  
 385 390 395 400  
 Glu Ile Met Gln His Lys Phe Phe Ala Gly Ile Val Trp Gln Asp Val  
 405 410 415  
 Tyr Gly Lys Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu  
 420 425 430  
 Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile Thr  
 435 440 445  
 Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Asp Cys Val Asp Asn Glu  
 450 455 460  
 Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Thr Ala  
 465 470 475 480